

FIGURE 1

[illegible]

FIGURE 2

<241 aa, 1 stop
 <MW: 26000, pI: 6.34, NX(S/T): 1
 <greatest homology to MMU82534_1 glucocorticoid induced TNFR related>
 <protein - may be human homolog of this mouse gene>
 <25-26 potential signal peptide cleavage site>
 <33 4 TNFR - Cys repeat domains>
 <146 potential N-linked glycosylation site>
 <162 start potential transmembrane domain>
 <180 end potential transmembrane domain>
 < 1 10 20 30 40 50 60 70
 < MAQHGMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGECCSEW
 < 71 80 90 100 110 120 130 140
 < DCMCVQPEFHCGDPCCTTCRHHPCCPPGQGVQSQGKFSFGFCIDCASGTFSGHGHCFTWDTCTQFGFL
 < 141 150 160 170 180 190 200 210
 < TVFPGKTHNAVCPGSPPAEPLGWLTVVLLAVAACVLLTSAQLGHTWQLRSQCMWPRETQLLEVP
 < 211 220 230 240
 < STEDARSCQFPEERGERSAEKGRLGLMW

FIGURE 3A

<consen01> 1 GGCACAGCACGGGGCGATGGGCGCGTTTCGGGGCCCTGTGCGGCCTGGCGC

<consen01> 51 TGCTGTGCGCGCTCAGCCTGGGTCAGCGCCCCACCGGGGT-CCCGGGTG

<consen01> 101 CGGCCCTGGGCGCCTCCTGCTTGGGACGGGAACGGACGCGCGCTGCTGCC

<consen01> 151 GGGTTCACACGACGCGCTGCTGCCGCGATTACCGGGCGAGGAGTGCTGT

<consen01> 201 TCCGAGTGGGACTGCATGTGTGTCCAGCCTGAATTCCACTGCGGAGACCC

0964397E.071100

FIGURE 3B

<consen01> 251 TTGCTGCACGACCTGCCGGCACCACCCTTGTCCTCCAGGCCAGGGGGTAC

<consen01> 301 AGTCCCAGGGGAAATTTCAGTTTGGCTTCCAGTGTATCGACTGTGCCTCG

<consen01> 351 GG-GACCTTCTCCGGGGGCCACGAAG--GCCACTGCAAACCTTGGACAGA

<consen01> 401 CTGCACCCAGTT-CGGG-TTCTCACTGTGTTCCCTGGGGAACAAGACCC

<consen01> 451 -ACAA-CGCTGTGTGCGTCCCAGGGTCCCCG-CCGGCAGAGCCGCTT-GG

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FIGURE 3C

<consen01> 501 GTGGCTGACCGTCGTCCTCCTGGCCGT-GGCCGCCTGCGTC-TCCTCCTG

<consen01> 551 ACCTCGGCCCAGCTTGGACTGCACATCTGGCAGCTGAGGAGTCAGTGCAT

<consen01> 601 GTGGCCCCGAGGTCTGTACAGCCTGGTGCGGGGAGGTGGGAGCATGGCT

<consen01> 651 GCCTGCTGACCGTGGCCCCCTGCATAGACCCAGCTGCTGCTGGAGGTGC

<consen01> 701 CGCCGTCGACCGAAGACGCCAGAAGCTGCCAGTTCCCCGAGGAAGAGCGG

<consen01> 751 GGCGAGCGATCGGCAGAGGAGAAGGGGCGGCTGGGAGACCTGTGGGTGTG

<consen01> 801 AGCCTGGCTGTCTCCGGGGCCACCGACCGCAGCCAGCCCCCTCCCCAGGA

<consen01> 851 GCTCCCCAGGCCCGCAGGGGCTCTGCGTTCTGCTCTGGGCCGGGCCCTGCT

<consen01> 901 CCCCTGGCAGCAGAAGTGGGTGCAGGAAGGTGGCAGTGACCAGCGCCCTG

<consen01> 951 GACCATGCAGTTC

00112026100

FIGURE 4

1 124TACAGAC GGGGCGATGG GCGCTTTTC GCGCTGTGCG TGCTGTGCG GCTGACCTG GCTGACGCG CACACCGGCG TCCCGGTGCG
 1 124TGTGCTG CCGCGTAC CCGCGACG CCGCGACG CCGCGACG CCGCGACG CCGCGACG CCGCGACG CCGCGACG CCGCGACG
 *44825.G1TR.f *orf
 *44825.f1
 101 GCGCTGTGCG GCGCTGTGCG TCGACGCG GCGCTGTGCG GCGCTGTGCG GCGCTGTGCG GCGCTGTGCG GCGCTGTGCG GCGCTGTGCG
 29 G P G R L L L G T G T D A R C C R V H T T R C C R D Y P G E E C C S
 *44825.p1
 201 CCGAGTGGGA CTGCACTGT GTGCACTGT GTGCACTGT GTGCACTGT GTGCACTGT GTGCACTGT GTGCACTGT GTGCACTGT
 GCGTCACTGT GCGTCACTGT GCGTCACTGT GCGTCACTGT GCGTCACTGT GCGTCACTGT GCGTCACTGT GCGTCACTGT
 63 E W D C H C V Q P E F H C G D P C C T T C R H H P C P P G Q G V Q
 301 GTCCGAGGCG AATTCAGTT TTGCTTCCA GTGATTCAG GTGATTCAG GTGATTCAG GTGATTCAG GTGATTCAG GTGATTCAG
 CAGGTGCGCG TTGATTCAG AATTCAGTT CACATAGCT CACATAGCT CACATAGCT CACATAGCT CACATAGCT CACATAGCT
 96 S Q G K F S P G P Q C I D C A S G T F S G Q H E G H C K P M T D C
 *44825.G1TR.x
 401 ACCGAGTTTC GGTTCCTAC TGTTCCTCT GCGAGACAG ACCGAGACG CTGTGCTCT CCGAGGTC CCGAGGTC CCGAGGTC
 TGGTCAAGC CCAAGAGTG ACAGAGGA CCGTCTGTC TGGTCTTC GACAGACGA GGTTCCTAC GGTTCCTAC GGTTCCTAC
 129 T Q P G P L T V F P G E Q D P Q R C V R F R V P A G R A A M V A D R
 501 GTGCTCTTC TGGCGTGGC GCGTCTGTC TCTCTCTAC CTGCGACCG CTGCGACCG CTGCGACCG CTGCGACCG CTGCGACCG
 CAGAGGAGG ACCGACCG CCGAGGAG AGGAGAGT GAGAGAGT GAGAGAGT GAGAGAGT GAGAGAGT GAGAGAGT
 163 R P P G R G R L R L L L T S A Q L G L H I W Q L R S Q C M W P R G
 601 TGTGTACAG CTGCTGTGCG GAGGTGCGA GATGCTGTC CTGCTGTGCG TGGCGTGGC TGGCGTGGC TGGCGTGGC TGGCGTGGC
 AGACAGTGT GACAGAGCG CCGTCACTGT CTGCTGTGCG GAGAGAGT GAGAGAGT GAGAGAGT GAGAGAGT GAGAGAGT
 196 L S Q P G A G R W E H G C L L T V A P L H R P S C C M R C R A R P
 701 AAGAGGCGAG AAGCTGCGAG TTCCCGGAG AGAGCGGAG CAGAGAGT CAGAGAGT CAGAGAGT CAGAGAGT CAGAGAGT
 TTCTGCGTTC TTGAGAGGTC AAGGCTGTC TTCTGCGCG TTCTGCGCG TTCTGCGCG TTCTGCGCG TTCTGCGCG
 229 K T P E A A S S P R K S G A S D R Q R R R G G W E T C G C E P G C P
 801 CTGCGGCGCG ACCGACCGA CCGAGCGCT CCGAGCGCT CCGAGCGCT CCGAGCGCT CCGAGCGCT CCGAGCGCT
 GAGCGCGCG TGGTGTGCT GAGCGCGCT GAGCGCGCT GAGCGCGCT GAGCGCGCT GAGCGCGCT GAGCGCGCT
 263 P G P P T A A S P S P G A P Q A A G A L R S A L G R A L L P W Q Q
 *44825.f2
 901 GAGTGTGCG CAGGAGGTC GAGTGTGCG GCGCTGTGCG CAGTGTGCG CAGTGTGCG CAGTGTGCG CAGTGTGCG
 CTTGAGGAG CTTGAGGAG CTTGAGGAG CTTGAGGAG CTTGAGGAG CTTGAGGAG CTTGAGGAG CTTGAGGAG
 296 K W V Q E G G S D Q R P G P C S S X A G X A
 *44825.f1

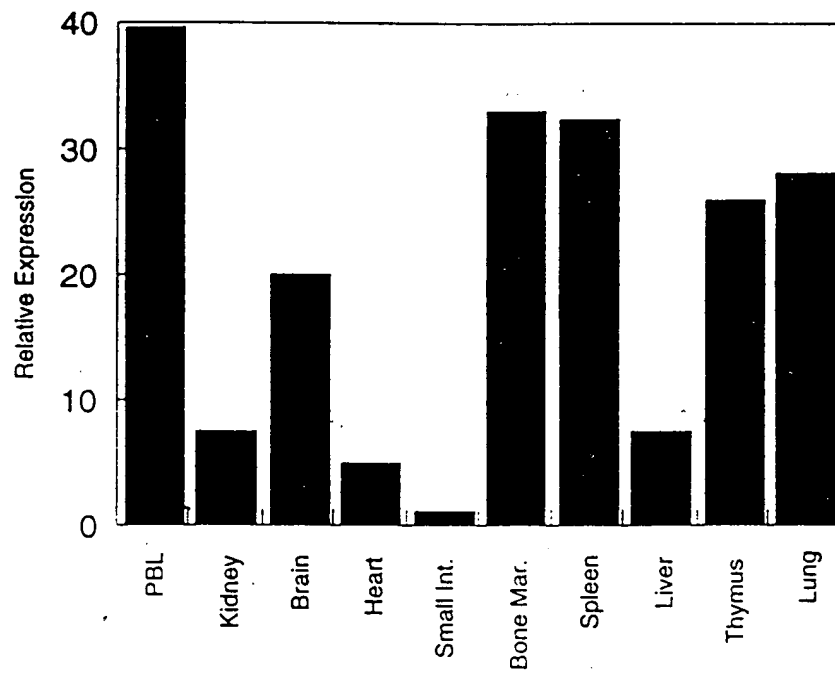
Fig. 5A

1 CAGCTCTCAT TTCTCCAAA ATCTGTTTGA GCCACTTGA AATATGCTT TTAAGCCATT CAACAACCTA AGCAGCTCAG AGATCATCTT GGAAGCTGTG
 1 CTGAGAGTA AAGAGGTTT TACACAACT CCGTGAACCT TTATACCGA AATGCGTAA GTTCTGAGT TCCTGAGTC TCTAGTAGGA CCTGACACAC
 MetCysLeus erHisLeuGI uasnMetPro LeuserHis erArgThrGI nGlyAlaGln ArgSerSert rPlysLeuTrp
 101 GCTCTTTTGC TCAATAGTTA TCTTGCTATT TCTTTGCTCC TTCAAGTTGC TAATCTTTAT TTTCTCCAA TTAGAGACTG CTNAGGAGCC CTGATATGGCT
 28 CGAGAAAACG AGTTATCAAT ACAACGATAA AGAACGAGG AACTCAACCG ATTAGAATA AAAAGAGGT AATCTCTGAC GATTCCTCGG CACATACCGA
 LeuPheCys SerileValM etLeuLeuPh eLeuCysSer PheSerTrpL euilePheII ePheLeuGln LeuGluThra laLysGluPr oCysMetAla
 201 AAGTTTGGAC CATTACCTC AATACCTC AATAGGCAA ATGGCATCTT CTGAACCTCC TTGCGTAAAT AAGCTGTCTG ACTGGAAGCT GGAGATACCT CAGAAATGGCT
 TTCAAAACCTG GTAAATGGAG TTTTACCGTT TACCGTAGAA GACTTGGAGG AAGCGACTTA TTCCACAGAC TCACCTTCGA CCTCTATGAA GTCTTACCGA
 61 LysPheGlyP roLeuProSe rLysTrpGln MetAlaSerS erGluProPr oCysValasn LysValserA sptRlysLe uGluileLeu GlnasnGlyLeu
 301 TATATTTAAT TTATGGCAA GTGGCTCCA ATGCCAACTA CAATGATGTA CCTCTTTTTC AGCTCGGCT CTATAAAAAC AAGACATGA TACAAACTCT
 ATATAAATA AATACCGGTT CACCGAGGTT TACCTTCAAT GTTACTACAT CCAGGAAAC TCCACGCCGA CATATTTTTC TTTCTGACT ATCTTTGACA
 95 TyrLeuII eTyGlyGln ValalaProA snAlaasnTy rAsnaspVal AlaProPheC luValargLe uTyRlysasn LysaspMetI leGlnThrLeu
 401 AACAAACAA TCTAAATCC AAAATGAGG AGGACTTAT GAATTCATG TTGGGACAC CATAGACTTG ATATTCAACT CTGAGCATCA GGTCTTAAAA
 TTGTTTGTTC AGATTTTAGG TTTTACATCC TCCCTGATA CTTAACGTAC AACCCCTGTC GTATCTGAAC TATAAGTTGA GACTCGTAGT CCAAGATTTT
 128 ThrAsnLys SerLysileG lnaasnValGI yGlyThry: GluLeuHisv alGlyaspTh rIleaspLeu IlePheAsns erGluHisGI nValleuLys
 501 AATAAATACAT ACTGGGGTAT CATTTTACTA GCAATCCCTC AATTCATCTC CTAGACACTT GATTTGATCT CCTCATTTCC TTACAGCACAT GTAGAGGTGC
 TTATATGTA TGACCCCAT GTAATATGAT CGTTAGGGG TTAAGTAGAG GATCTCTGAA CTAAACTAGA GGAGTNAAGG AAGTGGTCTA CATCTCCACG
 161 AsnAsnThrt yTrpGlyII eileLeuLeu AlaasnProG lnPheilese rAH
 601 CAGTGGGTGG ATTGGAGGGA GAAGATATT CTTCATATAA GTTGTCTGT CTACAAAAT CAACACAAC AGAATCTCTC TGCACGTGAA TTTTCATCTA
 GTCACCCACC TAACCTCCCT CTTCATATAA GTTAAAGATCT CAACAGACA GATGTTTTTA GTTGTTTTC TCTTGAGGAG ACGTGCACCTT AANAAGTAGAT
 701 TCATGCCCTAT CTGAAGAGA CTCAGGGGAA GAGCCAAAGA CTTTGTGTTG GATCTGCAGA AATACTTCAT TAATCCATGA TAAACAAAT ATGGATGACA
 AGTAGCGGATA GACTTTCTCT GACTCCCTTT CTCGGTTTCT GAAGACCAAC CTAGACCTCT TTATGAAGTA ATTAGGTACT ATTTGTTTA TACCTACTGT
 801 GAGCACATGT CTTTTTCAA GAATCTTTAT CTAAATCTTG AATTCATGAG TGGAAAATG GAGTCTTATT CCCATGGAG ATTTACCTGG TATGCAAAAA
 CTCCTGTACA CGAAAGTTT CTTAGAATA GATTAAGAAC TTAAGTACTC ACCTTTTAC CTCACATAA GGGTACCTTC TAAATGGACC ATACGTTTTT
 901 GATCTCTGGG CAGTAGCCCTG CTTTGTCTCT CATATTTCTT GCTGTCTGTA ATTCATCTCT CTCACTACTC CATCTTCTGA GACCTCCCA ATAAAAAGTA
 CCTAGACCCC CTCATCGGAC CGAAACAAGA GTATAACAAG TTAGATATG GTGCTGTTAG AGATRAAGA ACAATCTGAG AACTATTGGA ATAGAGGTAC
 1001 GACTGATAGG ATGGCCACAG ATATGCCCTAC CATACCCCTAC TTTAGATATG GTGCTGTTAG AGATRAAGA ACAATCTGAG AACTATTGGA ATAGAGGTAC
 CTCACATATCC TACCGGTCTC TATACGGATG CTATGGGAT: AATCTATAC CACCACAATC TTCTATTCT TCTTAGACTC TTGATAACCT TATCTCCATG

Fig. 5B

1901 TTTTAAAAATAT TTATGGGATAT TTCTGAAAG CTCGATTATC TTAAATAATA TTACATGTAA AGCT
AAATTTTATA AATACCTATA AACACTTTTC GACGTAATAC AATTTATAT AATGTACATT TCGA

Fig. 6

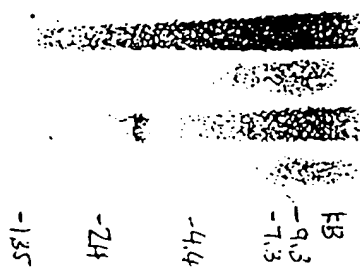


007720 2/5/99

Cell Type	Treatment	Relative mRNA expression (approx.)
T cells	(-)	1
	anti-CD3	77
	PHA	35
Monocytes	(-)	14
	LPS	23

Fig. 7

Fetal
Human



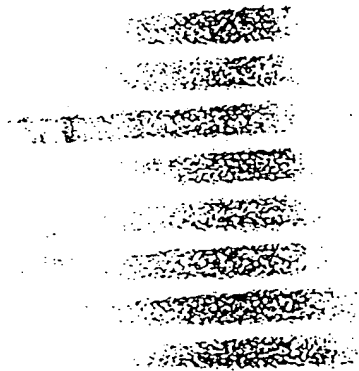
Kidney
Liver
Lung
Brain

Human
Adult



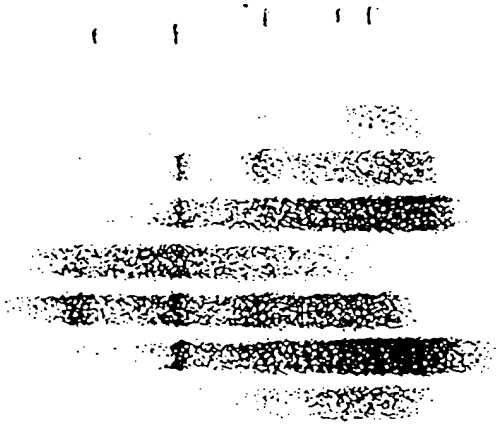
Pancreas
Kidney
Sk. Muscle
Liver
Lung
Placenta
Brain
Heart

Human
Adult



PBL
Colon
SM. INTEST
Ovary
Testis
prostate
Thymus
Spleen

Cancer



G-361
A549
SW480
Raji
MOLT-4
K-562
Hela S3
HL-60

Fig. 8

09613972.071100

0011397.01100

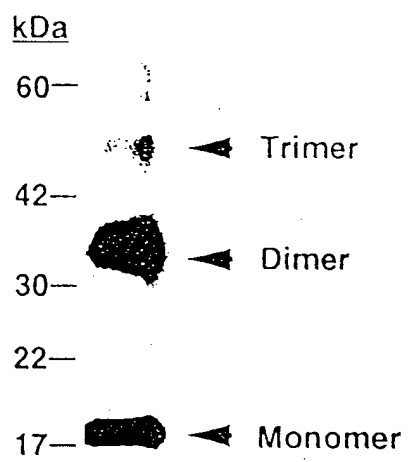


Fig. 9

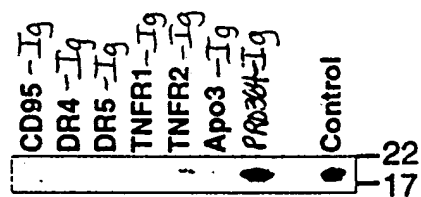


Fig. 10

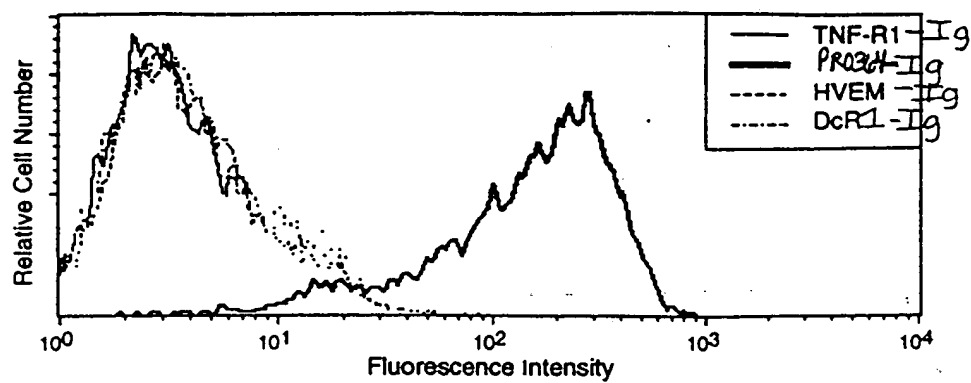


Fig. 11A

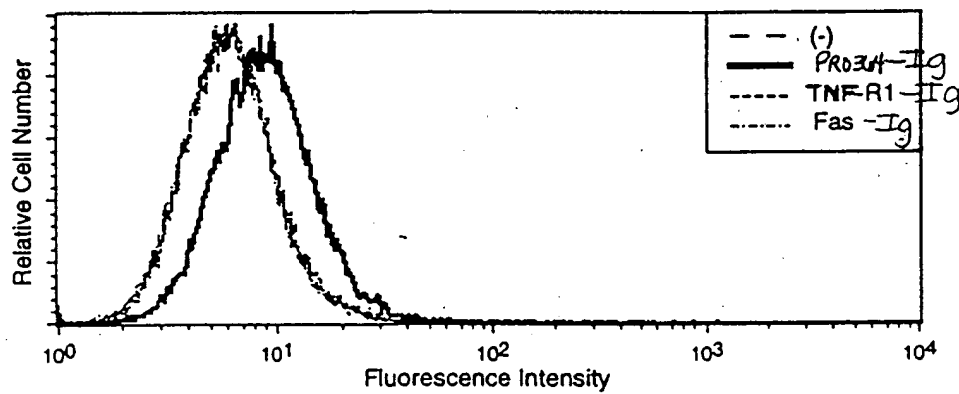


Fig. 11B

001120-2265T960

glt^r TNF H10g
PIN192

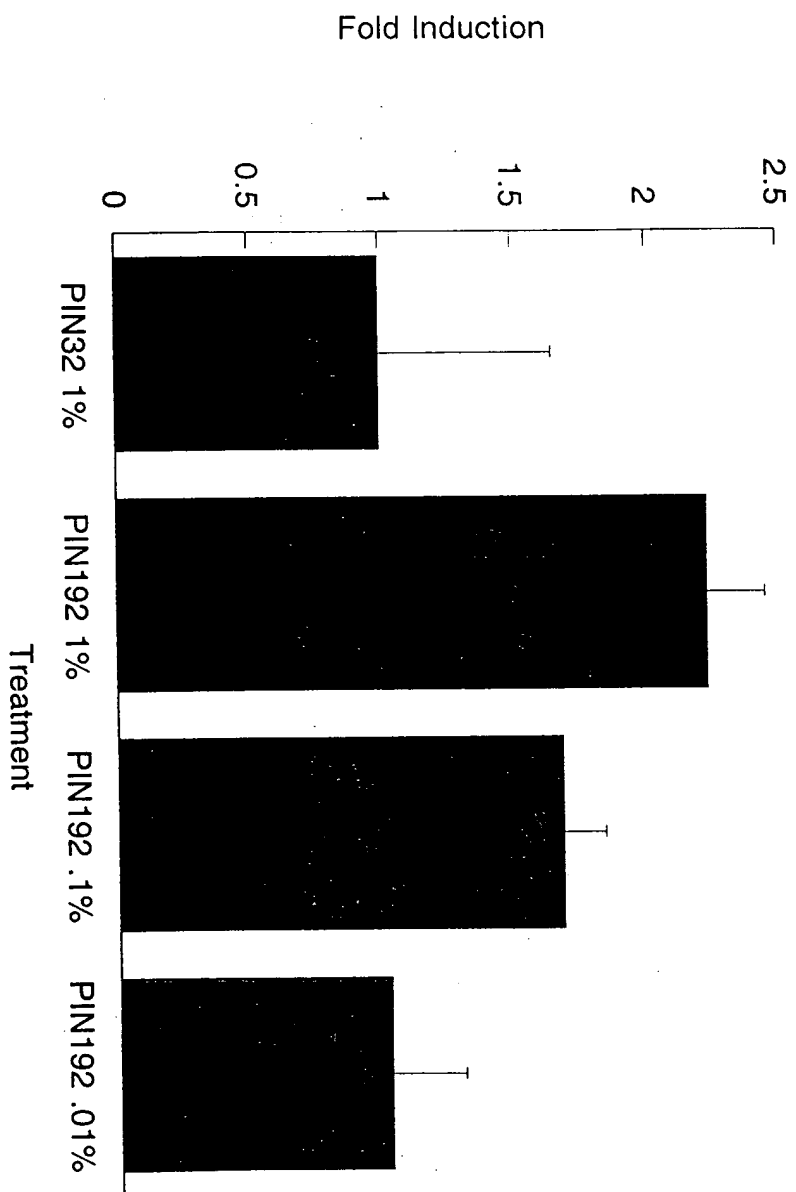


FIG. 12

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